

WE CLAIM:

1. A method of selecting a plant having enhanced transpiration efficiency, comprising detecting a genetic marker for transpiration efficiency which marker comprises a nucleotide sequence linked genetically to an *ERECTA* locus in the genome
5 of the plant and selecting a plant that comprises or expresses the genetic marker.
2. The method according to claim 1 wherein the genetic marker comprises an *ERECTA* allele or *erecta* allele, or a protein-encoding portion thereof.
- 10 3. The method according to claim 2 wherein the genetic marker comprises a nucleotide sequence having at least about 55% overall sequence identity to at least about 20 nucleotides in length of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11 to 19 or 21 to 44 or a complementary sequence thereto.
- 15 4. The method according to claim 2 or 3 wherein the genetic marker comprises a nucleotide sequence selected from the group consisting of:
 - (a) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44;
 - 20 (b) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45; and
 - 25 (c) a sequence complementary to (a) or (b).
- 30

5. The method according to any one of claims 1 to 4 wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, rice, sorghum, wheat and maize.
6. The method according to any one of claims 1 to 5 comprising linking the
5 transpiration efficiency phenotype of the plant to the expression of the marker in the plant.
7. The method according to any one of claims 1 to 5 comprising linking a structural polymorphism in DNA to a transpiration efficiency phenotype in the plant.
- 10 8. The method according to claim 7 wherein the polymorphism is determined by a process comprising detecting a restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), single strand chain polymorphism (SSCP) or microsatellite analysis.
- 15 9. The method according to any one of claims 1 to 8 comprising hybridizing a probe or primer of at least about 20 nucleotides in length from any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11 to 19 or 21 to 44 or a complementary sequence thereto to genomic DNA from the plant, and detecting the hybridization using a detection means.
- 20 10. The method according to any one of claims 1 to 9 wherein the selected plant has enhanced transpiration efficiency compared to a near-isogenic plant that does not comprise or express the genetic marker.
- 25 11. A method of selecting a plant having enhanced transpiration efficiency, comprising:
- (a) screening mutant or near-isogenic or recombinant inbred lines of plants to segregate alleles at an *ERECTA* locus;
 - (b) identifying a polymorphic marker linked to said *ERECTA* locus; and
 - 30 (c) selecting a plant that comprises or expresses the marker.

12. A method of modulating the transpiration efficiency of a plant comprising introducing an isolated *ERECTA* gene or an allelic variant thereof or the protein-encoding region thereof to a plant and selecting a plant having a different transpiration efficiency compared to a near-isogenic plant that does not comprise the introduced
5 *ERECTA* gene or allelic variant or protein-encoding region.

13. The method according to claim 12 wherein the *ERECTA* gene or allelic variant or protein-encoding region comprises a nucleotide sequence selected from the group consisting of:

- 10 (c) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19; SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID
15 NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38; SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44; and
- 20 (d) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45.

25 14. The method according to claim 12 or 13 wherein the plant is selected from the group consisting of *Arabidopsis thaliana*, rice, sorghum, wheat and maize.

15. The method according to any one of claims 12 to 14 wherein the *ERECTA* gene or allelic variant or protein-encoding region is introduced to the plant by a process
30 comprising introgression.

16. The method according to any one of claims 12 to 14 wherein the *ERECTA* gene or allelic variant or protein-encoding region is introduced to the plant by a process comprising transforming plant material with a gene construct comprising the gene or allelic variant or protein-encoding region thereof.

5

17. The method according to any one of claims 12 to 16 further comprising expressing the introduced gene or allelic variant or protein encoding region in the plant.

18. The method according to any one of claims 12 to 17 wherein transpiration
10 efficiency is enhanced in the plant.

19. The method of claim 18 wherein the transpiration efficiency is enhanced as a consequence of the ectopic expression of an *ERECTA* allele or the protein-encoding region thereof in the plant.

15

20. The method according to any one of claims 12 to 17 wherein transpiration efficiency is reduced in the plant.

21. The method of claim 20 wherein the transpiration efficiency is reduced as a
20 consequence of reduced expression of an *ERECTA* allele in the plant.

22. A plant having modified transpiration efficiency compared to a near-isogenic plant wherein said plant is produced by a process comprising performing the method according to any one of claims 12 to 21.

25

23. The plant of claim 22 selected from the group consisting of a rice plant, a wheat plant and a maize plant.

24. An isolated *ERECTA* gene from wheat comprising a nucleotide sequence
30 selected from the group consisting of:

- (i) a sequence selected from the group consisting of: SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19;
- (ii) a sequence encoding the amino acid sequence set forth in SEQ ID NO: 20; and
- 5 (iii) a sequence that is complementary to (i) or (ii).

25. An isolated *ERECTA* gene from maize comprising a nucleotide sequence selected from the group consisting of:

- (i) a sequence selected from the group consisting of: SEQ ID NO: 21, SEQ ID NO: 10 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44;
- 15 (ii) a sequence encoding the amino acid sequence set forth in SEQ ID NO: 45; and
- (iii) a sequence that is complementary to (i) or (ii).

26. A gene construct comprising the isolated *ERECTA* gene according to claim 24 or 25 operably in connection with a promoter sequence that is operable in a plant.

20

27. Use of an isolated *ERECTA* gene or allelic variant or protein-encoding region thereof in the preparation of a genetic construct for modulating the transpiration efficiency of a plant.

25 28. Use according to claim 27 wherein the *ERECTA* gene or allelic variant or protein-encoding region comprises a nucleotide sequence selected from the group consisting of:

- (a) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19; SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44;

30

NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44; and

- (b) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45.

10

29. A method of identifying a gene that determines the transpiration efficiency of a plant comprising:

- (a) identifying a locus associated with genetic variation in transpiration efficiency in the plant;
- 15 (b) identifying a gene or allele that is linked to said locus, wherein said gene or allele is a candidate gene or allele for determining the transpiration efficiency of a plant; and
- (c) determining the transpiration efficiencies of a panel of plants, wherein not all members of said panel comprise or express said gene or allele, and wherein
- 20 variation in transpiration efficiency between the members of said panel indicates that said gene is involved in determining transpiration efficiency.

30. A method of identifying a gene that determines the transpiration efficiency of a plant comprising:

- 25 (a) identifying a locus associated with genetic variation in transpiration efficiency in a plant;
- (b) identifying multiple alleles of a gene that is linked to said locus, wherein said gene is a candidate gene involved for determining the transpiration efficiency of a plant; and
- 30 (d) determining the transpiration efficiencies of a panel of plants, wherein each member of said panel comprises at least one of said multiple alleles, wherein

transpiration efficiency between the members of said panel indicates that said gene is involved in determining transpiration efficiency.

31. A method of increasing the resistance of a plant to an environmental stress
5 comprising enhancing the level of expression of an *ERECTA* gene or allelic variant thereof or protein encoding region thereof in said plant.

32. A method of increasing seed or grain weight in a plant comprising enhancing
the level of expression of an *ERECTA* gene or allelic variant thereof or protein
10 encoding region thereof in said plant.

33. A method of increasing the number of seeds produced by a plant comprising
enhancing the level of expression of an *ERECTA* gene or allelic variant thereof or
protein encoding region thereof in said plant.

15 34. The method of any one of claims 31-33, the level of expression is enhanced by introducing an *ERECTA* gene or allelic variant thereof or the protein encoding region thereof to a plant.

20 35. The method of claim 34 wherein the *ERECTA* gene or allelic variant or protein-encoding region comprises a nucleotide sequence selected from the group consisting of:

(a) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44; and

25
30

- (b) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45.

5

36. A plant produced by the method of any one of claims 31 to 34.